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 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Jan 25  BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS  3  Jan 29  FSTA has been reloaded and moves to weekly updates
 NEWS  4  Feb 01  DKILIT now produced by FIZ Karlsruhe and has a new update
                  frequency
 NEWS  5  Feb 19  Access via Tymnet and SprintNet Eliminated Effective 3/31/02
 NEWS  6  Mar 08  Gene Names now available in BIOSIS
 NEWS  7  Mar 22  TOXLIT no longer available
 NEWS  8  Mar 22  TRCTHERMO no longer available
 NEWS  9  Mar 28  US Provisional Priorities searched with P in CA/CAplus
                  and USPATFULL
 NEWS 10  Mar 28  LIPINSKI/CALC added for property searching in REGISTRY
 NEWS 11  Apr 02  PAPERCHEM no longer available on STN.  Use PAPERCHEM2 instead.
 NEWS 12  Apr 08  "Ask CAS" for self-help around the clock
 NEWS 13  Apr 09  BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS 14  Apr 09  ZDB will be removed from STN
 NEWS 15  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS 16  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS 17  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS 18  Apr 22  Federal Research in Progress (FEDRIP) now available

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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=> e perlin m/au
E1            4      PERLIN JONATHAN B/AU
E2           12      PERLIN L/AU
E3           56 --> PERLIN M/AU
E4            2      PERLIN M D/AU
E5           52      PERLIN M H/AU
E6            2      PERLIN M J/AU
E7           19      PERLIN M L/AU
E8            1      PERLIN M P/AU
E9            6      PERLIN M S/AU
E10          27      PERLIN M W/AU
E11           5      PERLIN MARK/AU
E12          11      PERLIN MARK W/AU

=> e
E13          11      PERLIN MICHAEL H/AU
E14           6      PERLIN MICHAEL L/AU
E15           1      PERLIN P/AU
E16           1      PERLIN R/AU
E17           5      PERLIN R R/AU
E18          24      PERLIN S/AU
E19           8      PERLIN S A/AU
E20           8      PERLIN S I/AU
E21           4      PERLIN S J/AU
E22           5      PERLIN S M/AU
E23           2      PERLIN SUSAN A/AU
E24           2      PERLIN T/AU

=> s e3, e10, e11, e12
L1           99 ("PERLIN M"/AU OR "PERLIN M W"/AU OR "PERLIN MARK"/AU OR "PERLIN
                MARK W"/AU)

=> s l1 and mixed
L2            2 L1 AND MIXED

=> duplicate remove l2
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L2
L3            1 DUPLICATE REMOVE L2 (1 DUPLICATE REMOVED)

=> d bib ab

L3   ANSWER 1 OF 1     MEDLINE                          DUPLICATE 1
AN   2001668388     MEDLINE
DN   21571107   PubMed ID: 11714147
TI   Linear mixture analysis: a mathematical approach to resolving
     mixed DNA samples.
```

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AU   Perlin M W; Szabady B
CS   Cybergenetics, Pittsburgh, PA 15213, USA.
SO   JOURNAL OF FORENSIC SCIENCES, (2001 Nov) 46 (6) 1372-8.
     Journal code: 0375370. ISSN: 0022-1198.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   Priority Journals
EM   200112
ED   Entered STN: 20011121
     Last Updated on STN: 20020123
     Entered Medline: 20011207
AB   With the advent of PCR-based STR typing systems, mixed samples
     can be separated into their individual DNA profiles. Quantitative peak
     information can help in this analysis. However, despite such advances,
     forensic mixture analysis still remains a laborious art, with the high
     cost and effort often precluding timely reporting. We introduce here a new
     automated approach to resolving forensic DNA mixtures. Our linear mixture
     analysis (LMA) is a straightforward mathematical approach that can
     integrate all the quantitative PCR data into a single rapid computation.
     LMA has application to diverse mixture problems. As demonstrated here on
     laboratory STR data, LMA can assess the quality and utility of its
     solutions. Such rapid and robust methods for computer-based analysis of
     DNA mixtures may help in reducing crime.


=> s l1 and (pcr or rflp or repeat)
L4          21 L1 AND (PCR OR RFLP OR REPEAT)

=> s l1 and (pcr or rflp or snp or repeat)
L5          21 L1 AND (PCR OR RFLP OR SNP OR REPEAT)

=> duplicate remove l5
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L5
L6           14 DUPLICATE REMOVE L5 (7 DUPLICATES REMOVED)

=> d 1-14 bib ab

L6   ANSWER 1 OF 14     MEDLINE                          DUPLICATE 1
AN   2002199470      IN-PROCESS
DN   21929801   PubMed ID: 11933190
TI   Determining sequence length or content in zero, one, and two dimensions.
AU   Perlin Mark W; Szabady Beata
CS   Cybergenetics, Pittsburgh, Pennsylvania.
SO   HUMAN MUTATION, (2002 Apr) 19 (4) 361-73.
     Journal code: 9215429. ISSN: 1098-1004.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   IN-PROCESS; NONINDEXED; Priority Journals
ED   Entered STN: 20020405
     Last Updated on STN: 20020405
AB   High-throughput assays are essential for the practical application of
     mutation detection in medicine and research. Moreover, such assays should
     produce informative data of high quality that have a low-error rate and a
     low cost. Unfortunately, this is not currently the case. Instead, we
     typically witness legions of people reviewing imperfect data at
     astronomical expense yielding uncertain results. To address this problem,
     for the past decade we have been developing methods that exploit the
     inherent quantitative nature of DNA experiments. By generating
     high-quality data, careful DNA-signal quantification permits robust
     analysis for determining true alleles and certainty measures. We will
     explore several assays and methods. In a one-dimensional readout, short
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tandem **repeat** (STR) data display interesting artifacts. Even with high-quality data, **PCR** artifacts such as stutter and relative amplification can confound correct or automated scoring. However, by appropriate mathematical analysis, these artifacts can be essentially removed from the data. The result is fully automated data scoring, quality assessment, and new types of DNA analysis. These approaches enable the accurate analysis of pooled DNA samples, for both genetic and forensic applications. On a two-dimensional surface (comprised of zero-dimensional spots) one can perform assays of extremely high-throughput at low cost. The question is how to determine DNA sequence length or content from nonelectrophoretic intensity data. Here again, mathematical analysis of highly quantitative data provides a solution. We will discuss new lab assays that can produce data containing such information; mathematical transformation then determines DNA length or content.
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L6 ANSWER 2 OF 14 MEDLINE DUPLICATE 2
AN 2001668388 MEDLINE
DN 21571107 PubMed ID: 11714147
TI Linear mixture analysis: a mathematical approach to resolving mixed DNA samples.
AU **Perlin M W**; Szabady B
CS Cybergenetics, Pittsburgh, PA 15213, USA.
SO JOURNAL OF FORENSIC SCIENCES, (2001 Nov) 46 (6) 1372-8. Journal code: 0375370. ISSN: 0022-1198.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200112
ED Entered STN: 20011121
Last Updated on STN: 20020123
Entered Medline: 20011207
AB With the advent of **PCR**-based STR typing systems, mixed samples can be separated into their individual DNA profiles. Quantitative peak information can help in this analysis. However, despite such advances, forensic mixture analysis still remains a laborious art, with the high cost and effort often precluding timely reporting. We introduce here a new automated approach to resolving forensic DNA mixtures. Our linear mixture analysis (LMA) is a straightforward mathematical approach that can integrate all the quantitative **PCR** data into a single rapid computation. LMA has application to diverse mixture problems. As demonstrated here on laboratory STR data, LMA can assess the quality and utility of its solutions. Such rapid and robust methods for computer-based analysis of DNA mixtures may help in reducing crime.

L6 ANSWER 3 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2000:466443 BIOSIS
DN PREV200000466443
TI Method and system for genotyping.
AU **Perlin, Mark W. (1)**
CS (1) 5904 Beacon St., Pittsburgh, PA, 15217 USA
PI US 6054268 April 25, 2000
SO Official Gazette of the United States Patent and Trademark Office Patents, (Apr. 25, 2000) Vol. 1233, No. 4, pp. No pagination. e-file. ISSN: 0098-1133.
DT Patent
LA English
AB The present invention pertains to a process which can be fully automated for accurately determining the alleles of genetic markers. More specifically, the present invention is related to performing **PCR** amplification on locations of DNA to generate a reproducible pattern, labeling the **PCR** products, converting the labels into a signal, operating on the signal, and then determining the genotype of the location of the DNA. An amplification can include multiple locations from the DNA

of one or more individuals. The invention also pertains to genetics applications and systems which can effectively use this genotyping information.

L6 ANSWER 4 OF 14 MEDLINE DUPLICATE 3
AN 1999455102 MEDLINE
DN 99455102 PubMed ID: 10523529
TI Using quality measures to facilitate allele calling in high-throughput genotyping.
AU Palsson B; Palsson F; **Perlin M**; Gudbjartsson H; Stefansson K; Gulcher J
CS deCODE Genetics, Inc., 110 Reykjavik, Iceland.
SO GENOME RESEARCH, (1999 Oct) 9 (10) 1002-12.
Journal code: CES; 9518021. ISSN: 1088-9051.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199912
ED Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991202
AB Currently, the main limitation in high-throughput microsatellite genotyping is the required manual editing of allele calls. Even though programs for automated allele calling have been available for several years, they have limited capability because accurate data could only be assured by manual inspection of the electropherograms for confirmation. Here we describe the development of a parametric approach to allele call quality control that eliminates much of the time required for manual editing of the data. This approach was implemented in an editing tool, Decode-GT, that works downstream of the allele calling program, TrueAllele (TA). Decode-GT reads the output data from TA, displays the underlying electropherograms for the genotypes, and sorts the allele calls into three categories: good, bad, and ambiguous. It discards the bad calls, accepts the good calls, and suggests that the user inspect the ambiguous calls, thereby reducing dependence on manual editing. For the categorization we use the following parameters: (1) the quality value for each allele call from TrueAllele; (2) the peak height of the alleles; and (3) the size of the peak shift needed to move peaks into the nearest bin. Here we report how we optimized the parameters such that the size of the ambiguous category was minimized, and both the number of miscalled genotypes in the good category and the useable genotypes in the bad category were negligible. This approach reduces the manual editing time and results in <1% miscalls.

L6 ANSWER 5 OF 14 MEDLINE DUPLICATE 4
AN 96026116 MEDLINE
DN 96026116 PubMed ID: 7485172
TI Toward fully automated genotyping: genotyping microsatellite markers by deconvolution.
AU **Perlin M W**; Lancia G; Ng S K
CS Computer Science Department, Carnegie Mellon University, Pittsburgh, PA 15213, USA.
NC R01 NS32084 (NINDS)
SO AMERICAN JOURNAL OF HUMAN GENETICS, (1995 Nov) 57 (5) 1199-210.
Journal code: 3IM; 0370475. ISSN: 0002-9297.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199511
ED Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951130
AB Dense genetic linkage maps have been constructed for the human and mouse

genomes, with average densities of 2.9 cM and 0.35 cM, respectively. These genetic maps are crucial for mapping both Mendelian and complex traits and are useful in clinical genetic diagnosis. Current maps are largely comprised of abundant, easily assayed, and highly polymorphic **PCR** -based microsatellite markers, primarily dinucleotide (CA)n **repeats**. One key limitation of these length polymorphisms is the **PCR** stutter (or slippage) artifact that introduces additional stutter bands. With two (or more) closely spaced alleles, the stutter bands overlap, and it is difficult to accurately determine the correct alleles; this stutter phenomenon has all but precluded full automation, since a human must visually inspect the allele data. We describe here novel deconvolution methods for accurate genotyping that mathematically remove **PCR** stutter artifact from microsatellite markers. These methods overcome the manual interpretation bottleneck and thereby enable full automation of genetic map construction and use. New functionalities, including the pooling of DNAs and the pooling of markers, are described that may greatly reduce the associated experimentation requirements.

L6 ANSWER 6 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:266918 BIOSIS
DN PREV199598281218
TI Towards fully automated genotyping: Use of an X linked recessive spastic paraplegia family to test alternative analysis methods.
AU Kobayashi, H.; Hoffman, E. P. (1); Matise, T. C.; **Perlin, M. W.**; Marks, H. G.
CS (1) Dep. Molecular Genetics Biochem., Human Genetics Pediatrics, Univ. Pittsburgh Sch. Med., Pittsburgh, PA 15261 USA
SO Human Genetics, (1995) Vol. 95, No. 5, pp. 483-490. ISSN: 0340-6717.
DT Article
LA English
AB Advances in dinucleotide-based genetic maps open possibilities for large scale genotyping at high resolution. The current rate-limiting steps in use of these dense maps is data interpretation (allele definition), data entry, and statistical calculations. We have recently reported automated allele identification methods. Here we show that a 10-cM framework map of the human X chromosome can be analyzed on two lanes of an automated sequencer per individual (10-12 loci per lane). We use this map and analysis strategy to generate allele data for an X-linked recessive spastic paraplegia family with a known PLP mutation. We analyzed 198 genotypes in a single gel and used the data to test three methods of data analysis: manual meiotic breakpoint mapping, automated concordance analysis, and whole chromosome multipoint linkage analysis. All methods pinpointed the correct location of the gene. We propose that multipoint exclusion mapping may permit valid inflation of LOD scores using the equation max LOD - (next best LOD).

L6 ANSWER 7 OF 14 MEDLINE DUPLICATE 5
AN 96015064 MEDLINE
DN 96015064 PubMed ID: 8530043
TI Rapid construction of integrated maps using inner product mapping: YAC coverage of human chromosome 11.
AU **Perlin M W**; Duggan D J; Davis K; Farr J E; Findler R B; Higgins M J; Nowak N J; Evans G A; Qin S; Zhang J; +
CS Computer Science Department, Carnegie Mellon University, Pittsburgh, Pennsylvania 15213, USA.
NC HG00856 (NHGRI)
MH00802 (NIMH)
SO GENOMICS, (1995 Jul 20) 28 (2) 315-27. Journal code: GEN; 8800135. ISSN: 0888-7543.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199602

ED Entered STN: 19960220
Last Updated on STN: 19980206
Entered Medline: 19960201

AB Inner product mapping (IPM) has been proposed as a hybridization-based method for achieving low-cost, high-throughput, high-resolution radiation hybrid (RH) mapping of clones. Using Alu-**PCR** products of chromosome 11-specific clones, we serially hybridized a set of RHs against gridded filters of YACs having an average size of 350 kb. We then combined these hybridization data with preexisting RH map data to build an inner product map. This binning of 865 YACs provides the first high-resolution large-scale (> twofold redundancy) clonal coverage of human chromosome 11 and is the first inner product map ever constructed. We verified the accuracy and precision of this chromosome 11 map by performing a novel likelihood analysis on independent YAC hybridization data. These results establish that IPM is a highly rapid, inexpensive, accurate, and precise large-scale long-range mapping method, particularly when preexisting RH maps are available, and that IPM can replace or complement more conventional short-range mapping methods. IPM may enable the rapid construction of sequence-ready maps and the binning of expressed sequences.

L6 ANSWER 8 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:476445 BIOSIS
DN PREV199598490745
TI Quantitative analysis of gel electrophoresis data for automated genotyping applications.
AU Richards, D. R.; **Perlin, M. W.**
CS Computer Sci. Dep., Carnegie Mellon Univ., Pittsburgh, PA USA
SO American Journal of Human Genetics, (1995) Vol. 57, No. 4 SUPPL., pp. A26.
Meeting Info.: 45th Annual Meeting of the American Society of Human Genetics Minneapolis, Minnesota, USA October 24-28, 1995
ISSN: 0002-9297.
DT Conference
LA English

L6 ANSWER 9 OF 14 MEDLINE DUPLICATE 6
AN 95029378 MEDLINE
DN 95029378 PubMed ID: 7942856
TI Toward fully automated genotyping: allele assignment, pedigree construction, phase determination, and recombination detection in Duchenne muscular dystrophy.
AU **Perlin M W**; Burks M B; Hoop R C; Hoffman E P
CS School of Computer Science, Carnegie Mellon University, Pittsburgh, PA 15213.
NC R01 NS32084 (NINDS)
SO AMERICAN JOURNAL OF HUMAN GENETICS, (1994 Oct) 55 (4) 777-87.
Journal code: 3IM; 0370475. ISSN: 0002-9297.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199410
ED Entered STN: 19941222
Last Updated on STN: 20000303
Entered Medline: 19941025

AB Human genetic maps have made quantum leaps in the past few years, because of the characterization of > 2,000 CA dinucleotide **repeat** loci: these **PCR**-based markers offer extraordinarily high PIC, and within the next year their density is expected to reach intervals of a few centimorgans per marker. These new genetic maps open new avenues for disease gene research, including large-scale genotyping for both simple and complex disease loci. However, the allele patterns of many dinucleotide **repeat** loci can be complex and difficult to interpret, with genotyping errors a recognized problem. Furthermore, the possibility of genotyping individuals at hundreds or thousands of

polymorphic loci requires improvements in data handling and analysis. The automation of genotyping and analysis of computer-derived haplotypes would remove many of the barriers preventing optimal use of dense and informative dinucleotide genetic maps. Toward this end, we have automated the allele identification, genotyping, phase determinations, and inheritance consistency checks generated by four CA **repeats** within the 2.5-Mbp, 10-cM X-linked dystrophin gene, using fluorescein-labeled multiplexed **PCR** products analyzed on automated sequencers. The described algorithms can deconvolute and resolve closely spaced alleles, despite interfering stutter noise; set phase in females; propagate the phase through the family; and identify recombination events. We show the implementation of these algorithms for the completely automated interpretation of allele data and risk assessment for five Duchenne/Becker muscular dystrophy families. The described approach can be scaled up to perform genome-based analyses with hundreds or thousands of CA-**repeat** loci, using multiple fluorophors on automated sequencers.

L6 ANSWER 10 OF 14 MEDLINE
AN 96039037 MEDLINE
DN 96039037 PubMed ID: 7584409
TI Intelligent DNA-based molecular diagnostics using linked genetic markers.
AU Pathak D K; Hoffman E P; **Perlin M W**
CS Department of Computer Science, Carnegie Mellon University, USA.
SO ISMB, (1994) 2 331-9.
Journal code: CCP; 9509125.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199512
ED Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951214
AB This paper describes a knowledge-based system for molecular diagnostics, and its application to fully automated diagnosis of X-linked genetic disorders. Molecular diagnostic information is used in clinical practice for determining genetic risks, such as carrier determination and prenatal diagnosis. Initially, blood samples are obtained from related individuals, and **PCR** amplification is performed. Linkage-based molecular diagnosis then entails three data analysis steps. First, for every individual, the alleles (i.e., DNA composition) are determined at specified chromosomal locations. Second, the flow of genetic material among the individuals is established. Third, the probability that a given individual is either a carrier of the disease or affected by the disease is determined. The current practice is to perform each of these three steps manually, which is costly, time consuming, labor-intensive, and error-prone. As such, the knowledge-intensive data analysis and interpretation supersede the actual experimentation effort as the major bottleneck in molecular diagnostics. By examining the human problem solving for the task, we have designed and implemented a prototype knowledge-based system capable of fully automating linkage-based molecular diagnostics in X-linked genetic disorders, including Duchenne Muscular Dystrophy (DMD). Our system uses knowledge-based interpretation of gel electrophoresis images to determine individual DNA marker labels, a constraint satisfaction search for consistent genetic flow among individuals, and a blackboard-style problem solver for risk assessment. We describe the system's successful diagnosis of DMD carrier and affected individuals from raw clinical data.

L6 ANSWER 11 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1994:525359 BIOSIS
DN PREV199497538359
TI Automated genotyping of dinucleotide **repeat** markers.
AU **Perlin, M. W. (1)**; Hoffman, E. P.

CS (1) Computer Sci., Carnegie Mellon Univ., Pittsburgh, PA USA
SO American Journal of Human Genetics, (1994) Vol. 55, No. 3 SUPPL., pp. A199.
Meeting Info.: 44th Annual Meeting of the American Society of Human Genetics Montreal, Quebec, Canada October 18-22, 1994
ISSN: 0002-9297.
DT Conference
LA English

L6 ANSWER 12 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1993:444537 BIOSIS
DN PREV199345080162
TI Detection of indicator bacteria and pathogens in water by polymerase chain reaction (**PCR**) and gene probe methods.
AU Atlas, R. M. (1); Bej, A. (1); Mahbubani, M. (1); Steffan, R. (1); **Perlin, M. (1)**; Dicesare, J.; Haff, L.
CS (1) Dep. Biol., Univ. Louisville, Louisville, KY USA
SO Mongkolsuk, S. [Editor]; Lovett, P. S. [Editor]; Trempy, J. E. [Editor]. (1992) pp. 219-223. Biotechnology and environmental science: Molecular approaches.
Publisher: Plenum Press 233 Spring Street, New York, New York, USA.
Meeting Info.: International Conference Bangkok, Thailand August 21-24, 1990
ISBN: 0-306-44352-X.
DT Article
LA English

L6 ANSWER 13 OF 14 MEDLINE DUPLICATE 7
AN 92152848 MEDLINE
DN 92152848 PubMed ID: 1785923
TI Detection of Giardia cysts by using the polymerase chain reaction and distinguishing live from dead cysts.
AU Mahbubani M H; Bej A K; **Perlin M**; Schaefer F W 3rd; Jakubowski W; Atlas R M
CS Department of Biology, University of Louisville, Kentucky 40292.
SO APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (1991 Dec) 57 (12) 3456-61.
Journal code: 6K6; 7605801. ISSN: 0099-2240.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199203
ED Entered STN: 19920405
Last Updated on STN: 19920405
Entered Medline: 19920316
AB A method was developed for the detection of Giardia cysts by using the polymerase chain reaction (**PCR**) and the giardin gene as the target. DNA amplification by **PCR**, using giardin DNA as the target, resulted in detection of both live and dead cysts. When giardin mRNA was used as the target, the ability to amplify cDNA by **PCR** depended on the mode of killing. Cysts killed by freezing were not detected by **PCR** when giardin mRNA was the target. Cysts killed by heating or exposure to monochloramine, however, gave positive detection signals for both DNA and giardin mRNA targets. The amount of giardin mRNA and total RNA was significantly increased in live cysts following the induction of excystation. Cysts killed by freezing, heating, or exposure to monochloramine did not show a change in RNA content. The detection of the giardin gene by **PCR** permits a sensitive and specific diagnosis for Giardia spp. Discrimination between live and dead cysts can be made by measuring the amounts of RNA or **PCR**-amplified product from the giardin mRNA target before and after the induction of excystation.

L6 ANSWER 14 OF 14 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1991:381182 BIOSIS

DN BR41:53572
TI DETECTION OF VIABLE LEGIONELLA AND GIARDIA USING **PCR** AND GENE PROBES.
AU MAHBUBANI M; BEJ A; **PERLIN M**; SCHAEFER F; ATLAS R M
CS UNIV. LOUISVILLE, LOUISVILLE, KY.
SO 91ST GENERAL MEETING OF THE AMERICAN SOCIETY FOR MICROBIOLOGY 1991, DALLAS, TEXAS, USA, MAY 5-9, 1991. ABSTR GEN MEET AM SOC MICROBIOL. (1991) 91 (0), 87.
CODEN: AGMME8.
DT Conference
FS BR; OLD
LA English

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---Logging off of STN---

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Executing the logoff script...

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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	17.46	17.67

STN INTERNATIONAL LOGOFF AT 15:20:17 ON 08 MAY 2002